

Claims

1. A primer pair selected from among pairs of primers capable of complementarily binding to human papillomavirus (HPV) genome and having nucleotide sequences represented by
5 SEQ ID Nos. 1 and 2, SEQ ID Nos. 3 and 4, SEQ ID Nos. 5 and 6, and SEQ ID Nos. 7 and 8.

2. A kit for detecting human papillomavirus (HPV) genome, comprising one or more primer pairs selected from among pairs of primers capable of complementarily binding
10 to the HPV genome and having nucleotide sequences represented by SEQ ID Nos. 1 and 2, SEQ ID Nos. 3 and 4, SEQ ID Nos. 5 and 6, and SEQ ID Nos. 7 and 8.

3. A method of detecting human papillomavirus (HPV) genome, comprising performing a polymerase chain reaction
15 for genomic DNA contained in a biological sample using one or more primer pairs selected from among pairs of primers capable of complementarily binding to the HPV genome and having nucleotide sequences represented by SEQ ID Nos. 1 and 2, SEQ ID Nos. 3 and 4, SEQ ID Nos. 5 and 6, and SEQ ID
20 Nos. 7 and 8.

4. The method as set forth in claim 3, wherein an HPV
11 L1 gene is detected using the primer pair having the

nucleotide sequences represented by SEQ ID Nos. 1 and 2.

5. The method as set forth in claim 3, wherein an HPV 16 L1 gene is detected using the primer pair having the nucleotide sequences represented by SEQ ID Nos. 3 and 4.

5 6. The method as set forth in claim 3, wherein an HPV 18 L1 gene is detected using the primer pair having the nucleotide sequences represented by SEQ ID Nos. 5 and 6.

 7. The method as set forth in claim 3, wherein an HPV 31 L1 gene is detected using the primer pair having the
10 nucleotide sequences represented by SEQ ID Nos. 7 and 8.

 8. The kit for detecting the HPV genome as set forth
in claim 2, further comprising one or more plasmids
selected from among pGEM-HPV11 L1, pGEM-HPV16 L1, pGEM-
HPV18 L1 and pGEM-HPV31 L1 as a positive control in order
15 to realize quantitative analysis.